Advanced Techniques in Biology & Medicine

Anaya-Munoz, Adv Tech Biol Med 2017, 5:3
DOI: 10.4172/2379-1764.1000233

Commentary OMICS International

Flattening and Unpacking Human Genetic Variation in Mexico, Postwar to the Present

Victor Hugo Anaya-Munoz*

Escuela Nacional de Estudios Superiores, Unidad Morelia; Universidad Nacional Autónoma de México (UNAM). Antigua Carretera a Pátzcuaro Nº 8701, Col. Ex-Hacienda de San José la huerta. C.P. 58190. Morelia, Michoacán, México

***Corresponding author:** Victor Hugo Anaya-Munoz, Escuela Nacional de Estudios Superiores, Unidad Morelia; Universidad Nacional Autónoma de México (UNAM). Antigua Carretera a Pátzcuaro Nº 8701, Col. Ex-Hacienda de San José la huerta. CP 58190. Morelia, Michoacán, México, Tel: +4436893500 (Ext. 80541); E-mail: victor_anaya@enesmorelia.unam.mx

Received date: June 19, 2017; **Accepted date:** June 21, 2017; **Published date:** June 28, 2017

Commentary

In July 2004 the Mexican government created the National Institute for Genomic Medicine (INMEGEN) as part of a National Platform aimed towards the development of a Mexican genomic medicine focused on the prevention of chronic deceases affecting the local population, by finding correlations between genetic markers and conditions such as diabetes and obesity. In Silva-Zolezzi et al. reported the results of a country-wide survey exploring the genetic diversity of the Mexican mestizo and arguing for the existence of "private alleles" and their possible relations to diseases catalogued as public health concerns [1]. A number of papers have been published since then, some of them including criticisms on the methodology used, the results presented, as well as the research's implications [2-8].

In a recent paper, Anaya-Muñoz, et al. has argued that two perspectives have characterized the exploration of Mexican genomic diversity from a biomedical point of view: what they call the "flattening" and the "unpacking" research strategies [9]. Each is characterized by methodological assumptions that permeate the sampling design, result analysis and conclusions drawn from the genomic (or genetic) explorations performed.

The flattening approach is represented by Silva-Zolezzi et al. [1], which reports low levels of genomic variation suggesting a high homogeneity among the Mexican mestizo populations, despite the documented anthropological, historical and pharmaco-genetical evidence that shows otherwise. The Mexican-mestizo is genetically composed by elements of Spanish, Indígena (represented by a single group) and African descent (on a lower proportion). The reported genomic composition confirms the official narratives of a mestizo nation with roots on three genetic origins (America, Europe and Africa), creating a historically inaccurate vision of the indígenas as a bio-social, monolithic construct. Blood sampling, next-generation sequencing, as well as a statistical toolbox, support these genomic findings; however, the most controversial point is the sampling strategy, based only on political and geographical criteria (namely, the federal states of Mexico).

The unpacking strategy, by contrast, aims to reveal the biological diversity, by way of implementing a complex array of multidisciplinary methodological criteria including linguistic categories, and historical, anthropological and demographic data. This broader disciplinary array informs not only sampling design but also analysis of results. The first Mexican pharmaco-genetic study of this sort was led by Ruben Lisker [10] and helped planning the malaria eradication campaign in the mid-1960s [11,12]. The most recent example of this perspective is the work of Moreno-Estrada et al. [13]. The methodological approaches used by Lisker fifty years ago, and Moreno-Estrada recently, help to exhibit a complex genetic structure that is not only biologically interesting, but also biomedically and therapeutically relevant in the treatment of complex diseases.

The point raised by Anaya-Muñoz et al. [9] makes the case for the foremost importance of the epistemological assumptions supporting pharmaco-genomic research. As they claim, "[s]cientists' choices […] have consequences not just for accounts of genetic variation in human populations, but on social, demographic and biomedical practices as well" (2017, 109).

References

1. Silva-Zolezzi I, Hidalgo-Miranda A, Estrada-Gil J, Fernandez-Lopez JC, Uribe-Figueroa L, et al. (2009) Analysis of genomic diversity in Mexican Mestizo populations to develop genomic medicine in Mexico. Proc Natl Acad Sci 106: 8611-8616.
2. García-Deister V, López-Beltrán C (2015) País de gordos/país de muertos: Obesity, death and nation in biomedical and forensic genetics in Mexico. Soc Stud Sci 45: 797-815.
3. García-Deister V (2014) Laboratory life of the Mexican Mestizo. In: Wade P, López-Beltrán C, Restrepo E, Santos RV (eds) Mestizo Genomics: Race Mixture, Nation, and Science in Latin America. Durham, NC: Duke University Press, pp: 161-182.
4. Ilin A, Raiko T (2010) Practical approaches to principal component analysis in the presence of missing values. J Mach Learn Res 11: 1957-2000.
5. López-Beltrán C, García-Deister V, Rios Sandoval M. (2014) Negotiating the Mexican mestizo: On the possibility of a national genomics. In: Wade P, López-Beltrán C, Restrepo E, Santos RV, editors. (eds) Mestizo Genomics: Race Mixture, Nation, and Science in Latin America. Durham, NC: Duke University Press, London.
6. Lopez-Beltran C, Deister VG (2013) Scientific approaches to the Mexican mestizo. Hist Cienc Saude Manguinhos 20: 391-410.
7. Suárez-Díaz E (2014) The long and winding road of molecular data in phylogenetic analysis. J Hist Biol 47: 443-478.
8. Santos RV, da Silva GO, Gibbon S (2015) Pharmacogenomics, human genetic diversity and the incorporation and rejection of color/race in Brazil. BioSocieties 10: 48-69.
9. Anaya-Muñoz VH, García-Deister V, Suárez-Díaz E (2017) Flattening and unpacking human genetic variation in Mexico, post-war to present. Sci Context 30: 89-112.
10. Lisker-Yourkowitzky R, Loria A, Strygler I (1960) Anemia Hemolítica Ligada a La Inestabilidad Del Glutation Reducido de Los Eritrocitos.
11. Suárez-Díaz E (2014) Indigenous populations in Mexico: Medical anthropology in the work of Ruben Lisker in the 1960s. Stud Hist Philos Biol Biomed Sci 47: 108-117.
12. Mateos G, Suárez E (2012) Mexican science during the Cold War: an agenda for physics and the life sciences. Ludus Vitalis 20: 47-69.

13. Moreno-Estrada A, Gignoux CR, Fernandez-Lopez JC, Zakharia F, Sikora M, et al. (2014) The genetics of Mexico recapitulates native American substructure and affects biomedical traits. Science 344: 1280-1285.